AMENDMENTS TO THE CLAIMS

IN THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) An isolated polypeptide comprising one or more of the amino acid motifs selected from the group consisting of a sequence with at least 80% identity to any of

(a) P-L-X-D-X(35,75)-R-R-X(8)- [YF]-X(2) -R-X(6)-T,

(b) C-X-D-X(3)-S-G-H-T or

(c) H-Y- [TS]-X-D- [VI]-X(3) - [FYI] -X(6) -F-X(2)-Y-H.

2. (Original) A polypeptide according to claim 1 that is derived from the group consisting of *Animalia*, *Alveolata* and *Kinetoplastida*.

3. (Currently Amended) A polypeptide according to claim 1 ~~or 2~~ selected from the group comprising any of the SEQ ID No. 1-11 or at least 70% similarity thereto.

4. (Currently Amended) A polypeptide according to claim 1 ~~or 2~~ comprising an amino acid sequence with at least 70 % similarity to any of the SEQ ID No. 12-22.

5. (Currently Amended) A polypeptide according to any one of the preceding ~~previous~~ claims comprising an amino acid sequence with at least 20 % identity to any of the SEQ ID No. 12- 22.

6. (Original) A polypeptide according to claim 5 comprising an amino acid sequence with at least 30 % identity to SEQ ID No. 12.

7. (Original) A polypeptide according to claim 5 comprising an amino acid sequence with at least 40 % identity to any of the SEQ ID No. 19-21.

8. (Currently Amended) A polypeptide according to any one of ~~the~~ claims 1-3 comprising an amino acid sequence with at least 22 % identity to SEQ ID No. 22.

9. (Currently Amended) A polypeptide according to ~~any one of the~~ claims 1-~~6~~ with sphingomyelin synthase activity.

10. (Currently Amended) A polypeptide according to ~~any one of the~~ claims 1-~~5 and 7~~ with ethanolamine phosphorylceramide synthase activity.

11. (Currently Amended) A polypeptide according to ~~any one of the~~ claims 1-~~5 and 8~~ with one or more of the activities selected from the group consisting of phosphatidylcholine:glycoprotein cholinephosphotransferase and phosphatidylcholine:glycolipid cholinephosphotransferase.

12. (Original) A nucleotide sequence selected from the group consisting of a nucleotide sequence coding for any of the amino acid sequences as described in claim 9 and an anti sense nucleotide sequence that is complementary thereto.

13. (Original) A nucleotide sequence selected from the group consisting of a nucleotide sequence coding for any of the amino acid sequences as described in claim 10 and an anti sense nucleotide sequence that is complementary thereto.

14. (Original) A nucleotide sequence selected from the group consisting of a nucleotide sequence coding for any of the amino acid sequences as described in claim 11 and an anti sense nucleotide sequence that is complementary thereto.

15. (Original) A plasmid comprising any of the nucleotide sequences described in any of the claims 12,13 or 14.

16. (Original) A vector comprising any of the nucleotide sequences described in any of the claims 12,13 or 14.

17. (Original) A (micro)organism or cell line in which any of the nucleotide sequences described in claim 12 was introduced.

18. (Original) A (micro)organism or cell line in which any of the nucleotide sequences described in claim 13 was introduced.

19. (Original) A (micro)organism or cell line in which any of the nucleotide sequences described in claim 14 was introduced.

20. (Original) A process for producing sphingomyelin synthase comprising the expression of any one of the nucleotide sequences described in claim 12 in a (micro)organism or cell line of claim 17 and the isolation of sphingomyelin synthase.

21. (Original) A process for producing sphingomyelin comprising the expression of the nucleotide sequences described in claim 12 in a (micro)organism or cell of claim 17 and the isolation of sphingomyelin.

22. (Original) Use of one of more of the nucleotide sequences of claim 12 to influence the reaction

$$CER + PC \leftrightarrow SM + DAG$$

in vivo or *in vitro*.

23. (Original) Use of one of more of the nucleotide sequences of claim 12 to identify or develop compounds influencing the reaction

$$CER+PC \leftrightarrow SM+DAG$$

in vivo or *in vitro*.

24. (Original) A process for producing ethanolamine phosphorylceramide synthase comprising the expression of any one of the nucleotide sequences described in claim 13 in a (micro)organism or cell line of claim 18 and the isolation of ethanolamine phosphorylceramide synthase.

25. (Original) A process for producing ethanolamine phosphorylceramide comprising the expression of the nucleotide sequences described in claim 13 in a (micro)organism or cell line of claim 18 and the isolation of ethanolamine phosphorylceramide.

26. (Original) Use of any one of the nucleotide sequences of claim 13 to influence the reaction

$$CER + PE \leftrightarrow EPC + DAG$$

in vivo or *in vitro*.

27. (Original) Use of any one of the nucleotide sequences of claim 13 to identify or develop compounds influencing the reaction

$$CER + PE \leftrightarrow EPC + DAG$$

in vivo or *in vitro*.

28. (Original) The application of the compounds of claim 23 or 27 in medical use.

29. (Original) The application of the compounds of claim 28 for the manufacture of medicaments treating a disease selected from the group consisting of cancer, metabolic diseases and diseases caused by parasites.

30. (Original) A process for producing phosphatidyl:glycoprotein cholinephosphotransferase or phosphatidyl:glycolipid cholinephosphotransferase comprising the expression of any one of the corresponding nucleotide sequences described in claim 14 in a (micro)organism or a cell line of claim 19 and the isolation of phosphatidyl:glycoprotein cholinephosphotransferase or phosphatidyl:glycolipid cholinephosphotransferase.

31. (Original) A process for producing phosphorylcholine-substituted glycoprotein or phosphorylcholine-substituted glycolipid comprising the expression of the corresponding nucleotide sequences described in claim 14 in a (micro)organism or cell of claim 19 and the isolation of phosphorylcholine-substituted glycoprotein or phosphorylcholine-substituted glycolipid.

32. (Original) Use of one of more of the nucleotide sequences of claim 14 to influence the reaction

glyco lipid/protein + PC ↔ PC-substituted glyco lipid/protein + DAG

in vivo or *in vitro*.

33. (Original) Use of one of more of the nucleotide sequences of claim 14 to identify or develop compounds influencing the reaction

glyco lipid/protein + PC ↔ PC-substituted glyco lipid/protein + DAG

in vivo or *in vitro*.

34. (Original) The application of the compounds of claim 33 in medical use.

35. (Original) The application of the compounds of claim 34 for the manufacture of a medicament treating a disease caused by parasitic nematodes.

36. (Original) A process to isolate candidates for functional genes of a previously unidentified enzyme with known activity from a huge database by combining at least four characteristics based on data from bio-informatics and from biochemistry, viz.
- presence of a sequence motif shared with previously identified enzymes having a related function
- biochemical function of the gene should be unknown until now
- no structural homologues in an organism that does not contain the enzyme
- ability to mediate a reaction catalysed by the unidentified enzyme upon its heterologous expression in an organism or cell lacking said enzyme activity.

37. (Original) A process to isolate candidates for functional genes according to claim 36 characterized by also considering the presence or non-presence of transmembrane domains depending on the working mechanism of the enzyme in relation to the membrane.

38. (Currently Amended) A method for determining whether a compound is capable of modulating an enzymatic activity displayed by a cell, said activity comprising an activity of an enzyme of the group of enzymes identified as sphingomyelin synthases, ethanolamine phosphorylceramide synthases, phosphatidylcholine:glycoprotein cholinephosphotransferase and phosphatidylcholine:glycolipid cholinephosphotransferase, said method comprising providing said

cell with a nucleic acid encoding a polypeptide according to any one of claims 1-4 and 9-11 ~~1-11~~, contacting said cell with said compound and determining whether said enzymatic activity is modulated.

39. (Original) A method according to claim 38 wherein said cell is deficient in sphingomyelin synthase activity.

40. (Original) A method according to claim 38 ~~or claim 39~~, wherein said cell is a cell of a eukaryotic micro-organism.

41. (Original) A method according to claim 40, wherein said cell is yeast cell.

42. (Currently Amended) A method according to ~~any one of~~ claims 38-~~41~~, wherein said polypeptide comprises a sequence as depicted in figure 8 or a functional part, derivative and/or homologue thereof.

43. (Original) A method according to claim 42, wherein said polypeptide comprises a sequence as depicted in figure 8A or a functional part, derivative and/or homologue thereof.

44. (Currently Amended) A method according to ~~any one of~~ claims 38-~~43~~, wherein said polypeptide is derived from a plasmodium.

45. (Original) A method according to claim 44, wherein said plasmodium sequence is a sequence as depicted in figure 8B or a functional part, derivative and/or homologue thereof.

46. (Currently Amended) A method according to ~~any one of~~ claims 38-~~45~~, wherein said compound comprises RNA.

47. (Currently Amended) Use of a nucleic acid encoding a polypeptide according to ~~any one of~~ claims 1-~~11~~, as a probe.

48. (Original) Use of an oligonucleotide specific for a nucleic acid sequence encoding a polypeptide as depicted in figure 8 or a functional part, derivative and/or homologue thereof, for detecting said sequence.

49. (Original) Use according to claim 47 or claim 48, for assessing whether a cell comprises sphingomyelin synthase activity.

50. (Currently Amended) Use of an inhibitor of a sphingomyelin synthase according to ~~any one of~~ claims 1~~-11~~, as a cell death promoter.

51. (Original) Use according to claim 50, wherein said cell is a cell of a parasite.

52. (Original) Use according to claim 50, wherein said cell is a human cell, preferably a tumor cell.

53. (Original) Use of a nucleic acid according to any one of claims 12-14, preferably comprising a nucleic acid sequence encoding a polypeptide as depicted in figure 8 or a functional part, derivative and/or homologue thereof for enhancing cell survival and/or cell growth.

54. (Currently Amended) A method for at least in part improving the yield of an secretion product of a cell comprising providing said cell with a polypeptide according to any one of claims 1-4 and 9-11 ~~1-11~~, or a nucleic acid according to any one of claims 12-14, preferably comprising a nucleic acid sequence encoding a polypeptide as depicted in figure 8 or a functional part, derivative and/or homologue thereof.

55. (Original) A method according to claim 54, wherein said cell is a cell of a eukaryotic micro-organism.

56. (Currently Amended) A method according to ~~any one of~~ claims 38 ~~38-46~~, further comprising providing said cell or a fraction thereof with a labelled substrate for said sphingomyelin synthase.

57. (Original) A method according to claim 56, further comprising harvesting sphingolipid from said cell or said fraction and detecting labelled sphingolipid.

58. (Currently Amended) A method according to claim ~~56 or~~ 57, further comprising detecting said labelled sphingolipid using (thin layer) chromatography or mass spectrometry.

59. (Currently Amended) A method for targeting a first polypeptide according to any one of claims 1-4 and 9-11 ~~1-11~~ to a different cellular compartment comprising providing a cytosolic part of said first polypeptide with a cellular compartment localization signal of a cytosolic part of a second polypeptide according to any one of claims 1-4 and 9-11 ~~1-11~~, wherein said first and said second polypeptide, when unmodified, reside in different cellular compartments.

60. (Original) A method according to claim 59, wherein said cytosolic part of said first polypeptide comprises the C-terminal end of said polypeptide.

61. (Original) A method according to claim 59 ~~or claim 60~~, wherein said cytosolic part of said second polypeptide comprises the C-terminal end of said polypeptide.

62. (Currently Amended) A method according to any one of claims 59 ~~59-61~~, wherein said cellular compartments comprises the plasma membrane, the endosomal compartment, the Golgi, the endoplasmatic reticulum or a combination thereof.

63. (Currently Amended) A method according to any one of claims 59 ~~59-62~~, wherein said cellular compartment localization signal of said second polypeptide replace the C- terminal cytosolic part of said first polypeptide.